



032301.230.SEQ.ST25.txt  
SEQUENCE LISTING

<110> FARWICK, Mike, et al.

<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE dead GENE

<130> 032301 WD 230

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 2381

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (259)..(2130)

<223>

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actgttgaag atgcaccaggc atctgagggt agcgaagaga tcaccagggt tgcggatact 1  
20

tctgaggacg ccgactctgc agatgcagac aacgcgagca atgtaatcaa tgagaatgag 1  
80

gactcctcgg aagggtgctaa ccagccttca aacgagtcat cctctacgga agccaaatcc 2  
40

ggcttcgatg cactcggc ctg cca gag cgt gta ctt gac gct gtg cgc aag 2  
91

Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys

1

5

10

gtg ggt tac gaa act cct tcc cca att cag gca caa acc atc cca atc 3  
39

Val Gly Tyr Glu Thr Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile

15

20

25

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ctc atg gag ggc cag gat gtt gtt ggt cta gca cag acc ggt acc ggt 3  
87 Leu Met Glu Gly Gln Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly  
30 35 40

aag act gca gct ttc gcg ctg cca atc ctt gcc cgt att gac aag tcc 4  
35 Lys Thr Ala Ala Phe Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser  
45 50 55

gtg cgc agc cca cag gca ctt gtg ctt gcc cct acc cgt gag cag gca 4  
83 Val Arg Ser Pro Gln Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala  
60 65 70 75

ctt cag gtt gct gac tcc ttc caa tcc ttc gct gac cac gtc ggt ggc 5  
31 Leu Gln Val Ala Asp Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly  
80 85 90

ctg aac gtt ctg cca atc tat ggt gga cag gct tac ggc att cag ctc 5  
79 Leu Asn Val Leu Pro Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu  
95 100 105

tct ggc ctg cgt cgt ggc gct cac atc gtc gtg ggt acc cca ggc cga 6  
27 Ser Gly Leu Arg Arg Gly Ala His Ile Val Val Gly Thr Pro Gly Arg  
110 115 120

atc atc gat cac ctc gaa aag ggc tcc ctg gat atc tcc gga ctg cgc 6  
75 Ile Ile Asp His Leu Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg

032301.230.SEQ.ST25.txt  
125                    130                    135

ttc ctc gtg ctc gat gaa gca gac gag atg ctg aac atg ggc ttc cag      7  
23

Phe Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln

140                    145                    150                    155

gaa gat gtc gag cgc atc ctc gag gac acc cca gac gag aag cag gtt      7  
71

Glu Asp Val Glu Arg Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val

160                    165                    170

gca cta ttc tcc gca acg atg cca aac ggc att cgt cgc ctg tcc aag      8  
19

Ala Leu Phe Ser Ala Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys

175                    180                    185

cag tac ctg aac aac cct gct gaa atc acc gtt aag tcc gag acc agg      8  
67

Gln Tyr Leu Asn Asn Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg

190                    195                    200

act aac acc aac atc acc cag cgc ttc ctc aac gtt gca cac cgc aac      9  
15

Thr Asn Thr Asn Ile Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn

205                    210                    215

aag atg gat gca ctg acc cgt att ctc gag gtc acc gag ttt gaa gca      9  
63

Lys Met Asp Ala Leu Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala

220                    225                    230                    235

atg atc atg ttc gtg cgc acc aag cac gaa act gaa gaa gtt gct gaa      10  
11

Met Ile Met Phe Val Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu

## 032301.230.SEQ.ST25.txt

240

245

250

aag ctc cgt gca cgc gga ttc tcc gca gca gcc atc aac ggc gac att 10  
 59

Lys Leu Arg Ala Arg Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile

255

260

265

gct cag gca cag cgt gag cgc acc gtc gac cag ctg aag gac ggc cgc 11  
 07

Ala Gln Ala Gln Arg Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg

270

275

280

ctg gac atc ctc gtt gca acc gac gtt gca gcc cgt ggt ctt gac gtt 11  
 55

Leu Asp Ile Leu Val Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val

285

290

295

gag cgc atc tcc cac gtg ctt aac ttc gac att cca aac gac acc gag 12  
 03

Glu Arg Ile Ser His Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu

300

305

310

315

tcc tac gtt cac cgc atc ggc cgc acc ggc cgt gca gga cgt acc ggc 12  
 51

Ser Tyr Val His Arg Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly

320

325

330

gag gca atc ctg ttc gtg acc cca cgt gag cgt cgt atg ctt cgc tcc 12  
 99

Glu Ala Ile Leu Phe Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser

335

340

345

atc gag cgc gca acc aac gca cca ctg cac gaa atg gaa ctg cca acc 13  
 47

032301.230.SEQ.ST25.txt

Ile Glu Arg Ala Thr Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr

350                    355                    360

gtc gat cag gtc aac gac ttc cgcc aag gtc aag ttc gct gac tcc atc 13  
95

Val Asp Gln Val Asn Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile

365                    370                    375

acc aag tcc ctc gag gac aag cag atg gac ctg ttc cgcc acc ctg gtc  
43 14

Thr Lys Ser Leu Glu Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val

aag gaa tac tcc cag gcc aac gac gtt cct cta gag gac atc gca gcg 14  
91

Lys Glu Tyr Ser Gln Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala

gca ctg gca acc cag gca cag tcc ggc gac ttc ctg ctc aag gag ctc 15  
39

Ala Leu Ala Thr Gln Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu

415                    420                    425

cca cca gag cg<sub>c</sub> cgt gag cg<sub>c</sub> aac gac cg<sub>c</sub> cgt cgt gac cg<sub>t</sub> gac ttc 15  
87

Pro Pro Glu Arg Arg Glu Arg Asn Asp Arg Arg Arg Arg Asp Arg Asp Phe

gac gac cgt ggt gga cgt gga cgc gac cgt gac cgt ggc gac cgc qqa 16

Asp Asp Arg Gly Gly Arg Gly Arg Asp Arg Arg Asp Glu

445 450

gat cat ggc tca ggc ttc gac

## 032301.230.SEQ.ST25.txt

83

Asp Arg Gly Ser Arg Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr

460

465

470

475

cgc ctc gca gtg ggc aag cgc cag cac atc cgc cca ggc gca atc gtt 17  
31

Arg Leu Ala Val Gly Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val

480

485

490

ggc gca ctt gcc aac gaa ggt ggc ctg aac tcc aag gac ttc ggc cgc 17  
79

Gly Ala Leu Ala Asn Glu Gly Leu Asn Ser Lys Asp Phe Gly Arg

495

500

505

atc acc atc gca gcc gac cac acc ctg gtt gaa ctg cca aag gat ctc 18  
27

Ile Thr Ile Ala Ala Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu

510

515

520

cca cag agc gtt ctt gac aac ctg cgc gac acc cgc atc tcc ggc cag 18  
75

Pro Gln Ser Val Leu Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln

525

530

535

ctc atc aac ata gaa cgc gac tcc ggt gga cgc cca cca cgc cgc ttc 19  
23

Leu Ile Asn Ile Glu Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe

540

545

550

555

gag cgc gat gac cgt ggc gga cgc ggc gga ttc cgc ggc gac cgt gat 19  
71

Glu Arg Asp Asp Arg Gly Gly Arg Gly Phe Arg Gly Asp Arg Asp

560

565

570

## 032301.230.SEQ.ST25.txt

gac cgc ggt gga cgt gga cgt gac cgt gac gat cgt gga agc cgt gga 20  
19

Asp Arg Gly Gly Arg Gly Arg Asp Arg Asp Arg Gly Ser Arg Gly

575

580

585

ggc ttc cgc ggt gga cgt gac cgt gat gat cgt ggc gga cgc ggt gga 20  
67

Gly Phe Arg Gly Gly Arg Asp Arg Asp Arg Gly Gly Arg Gly Gly

590

595

600

ttc cgc gga cgc gac gac cgc gga gac cgt ggt ggc cgt ggc ggt tac 21  
15

Phe Arg Gly Arg Asp Asp Arg Gly Asp Arg Gly Gly Arg Gly Tyr

605

610

615

cgt ggc gga cgc gac taagagttcg ttttagcttc agctcagggtt ttccgcctgag 21  
70

Arg Gly Gly Arg Asp

620

tctggtgctt agctagaaaa atccgttgct ctctcttac tgagagggca acggatttt 22  
30

tctgtttct taggctttgg ttcttgaaaa atcttggggg aggaattcta ggaacttaga 22  
90

gaagtaaatg atggtgcttc gaccgcagca ccatcgtaa gattctgacc aaagaagaga 23  
50

gcattgcgtt gctctctagt cagagtgcga g

23

81

&lt;210&gt; 2

&lt;211&gt; 624

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 2

032301.230.SEQ.ST25.txt

Met Pro Glu Arg Val Leu Asp Ala Val Arg Lys Val Gly Tyr Glu Thr  
1 5 10 15

Pro Ser Pro Ile Gln Ala Gln Thr Ile Pro Ile Leu Met Glu Gly Gln  
20 25 30

Asp Val Val Gly Leu Ala Gln Thr Gly Thr Gly Lys Thr Ala Ala Phe  
35 40 45

Ala Leu Pro Ile Leu Ala Arg Ile Asp Lys Ser Val Arg Ser Pro Gln  
50 55 60

Ala Leu Val Leu Ala Pro Thr Arg Glu Gln Ala Leu Gln Val Ala Asp  
65 70 75 80

Ser Phe Gln Ser Phe Ala Asp His Val Gly Gly Leu Asn Val Leu Pro  
85 90 95

Ile Tyr Gly Gly Gln Ala Tyr Gly Ile Gln Leu Ser Gly Leu Arg Arg  
100 105 110

Gly Ala His Ile Val Val Gly Thr Pro Gly Arg Ile Ile Asp His Leu  
115 120 125

Glu Lys Gly Ser Leu Asp Ile Ser Gly Leu Arg Phe Leu Val Leu Asp  
130 135 140

Glu Ala Asp Glu Met Leu Asn Met Gly Phe Gln Glu Asp Val Glu Arg  
145 150 155 160

Ile Leu Glu Asp Thr Pro Asp Glu Lys Gln Val Ala Leu Phe Ser Ala  
165 170 175

Thr Met Pro Asn Gly Ile Arg Arg Leu Ser Lys Gln Tyr Leu Asn Asn  
180 185 190

032301.230.SEQ.ST25.txt

Pro Ala Glu Ile Thr Val Lys Ser Glu Thr Arg Thr Asn Thr Asn Ile  
195 200 205

Thr Gln Arg Phe Leu Asn Val Ala His Arg Asn Lys Met Asp Ala Leu  
210 215 220

Thr Arg Ile Leu Glu Val Thr Glu Phe Glu Ala Met Ile Met Phe Val  
225 230 235 240

Arg Thr Lys His Glu Thr Glu Glu Val Ala Glu Lys Leu Arg Ala Arg  
245 250 255

Gly Phe Ser Ala Ala Ala Ile Asn Gly Asp Ile Ala Gln Ala Gln Arg  
260 265 270

Glu Arg Thr Val Asp Gln Leu Lys Asp Gly Arg Leu Asp Ile Leu Val  
275 280 285

Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Val Glu Arg Ile Ser His  
290 295 300

Val Leu Asn Phe Asp Ile Pro Asn Asp Thr Glu Ser Tyr Val His Arg  
305 310 315 320

Ile Gly Arg Thr Gly Arg Ala Gly Arg Thr Gly Glu Ala Ile Leu Phe  
325 330 335

Val Thr Pro Arg Glu Arg Arg Met Leu Arg Ser Ile Glu Arg Ala Thr  
340 345 350

Asn Ala Pro Leu His Glu Met Glu Leu Pro Thr Val Asp Gln Val Asn  
355 360 365

Asp Phe Arg Lys Val Lys Phe Ala Asp Ser Ile Thr Lys Ser Leu Glu  
370 375 380

032301.230.SEQ.ST25.txt

Asp Lys Gln Met Asp Leu Phe Arg Thr Leu Val Lys Glu Tyr Ser Gln  
385 390 395 400

Ala Asn Asp Val Pro Leu Glu Asp Ile Ala Ala Ala Leu Ala Thr Gln  
405 410 415

Ala Gln Ser Gly Asp Phe Leu Leu Lys Glu Leu Pro Pro Glu Arg Arg  
420 425 430

Glu Arg Asn Asp Arg Arg Arg Asp Arg Asp Phe Asp Asp Arg Gly Gly  
435 440 445

Arg Gly Arg Asp Arg Asp Arg Gly Asp Arg Gly Asp Arg Gly Ser Arg  
450 455 460

Phe Asp Arg Asp Asp Glu Asn Leu Ala Thr Tyr Arg Leu Ala Val Gly  
465 470 475 480

Lys Arg Gln His Ile Arg Pro Gly Ala Ile Val Gly Ala Leu Ala Asn  
485 490 495

Glu Gly Gly Leu Asn Ser Lys Asp Phe Gly Arg Ile Thr Ile Ala Ala  
500 505 510

Asp His Thr Leu Val Glu Leu Pro Lys Asp Leu Pro Gln Ser Val Leu  
515 520 525

Asp Asn Leu Arg Asp Thr Arg Ile Ser Gly Gln Leu Ile Asn Ile Glu  
530 535 540

Arg Asp Ser Gly Gly Arg Pro Pro Arg Arg Phe Glu Arg Asp Asp Arg  
545 550 555 560

Gly Gly Arg Gly Gly Phe Arg Gly Asp Arg Asp Asp Arg Gly Gly Arg  
565 570 575

032301.230.SEQ.ST25.txt

Gly Arg Asp Arg Asp Asp Arg Gly Ser Arg Gly Gly Phe Arg Gly Gly  
580 585 590

Arg Asp Arg Asp Asp Arg Gly Gly Arg Gly Gly Phe Arg Gly Arg Asp  
595 600 605

Asp Arg Gly Asp Arg Gly Gly Arg Gly Gly Tyr Arg Gly Gly Arg Asp  
610 615 620

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<212> DNA

<213> Corynebacterium glutamicum

<400> 3

gatctagaaa tccggcttcg atgcactc

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<210> 4

<211> 28

<212> DNA

<213> Corynebacterium glutamicum

<400> 4

ctaagcttcg acggttggca gttccatt

28